

JAN 1 1997

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Kirihara, J. A.
Hibberd, K. A.
Anthony, J. L.
- (ii) TITLE OF THE INVENTION: METHOD FOR ALTERING THE NUTRITIONAL
CONTENT OF PLANT SEED
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
(B) STREET: P.O. Box 2938
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
(F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Unknown
(B) FILING DATE: 09-DEC-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/112,245
(B) FILING DATE: 25-AUG-1993

(A) APPLICATION NUMBER: 07/508,045
(B) FILING DATE: 11-APR-1990

(A) APPLICATION NUMBER: 07/467,983
(B) FILING DATE: 22-JAN-1990
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Woessner, Warren D
(B) REGISTRATION NUMBER: 30,440
(C) REFERENCE/DOCKET NUMBER: 950.011US1
- (ix) TELECOMMUNICATION INFORMATION:
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TECH CENTER 600 230

RECEIVED

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAAUCUGGA	AAUGUAACUU	CUUAUUUCUG	GUUGGCCACA	UACAUCAACC	AUAUUAUUGA	60
GACCAACAAG	CAACAUAGAA	AGUGGAAUCC	AGUAGCAACA	ACAGAGCAAC	AAUGGCGACC	120
AAGAUUUUU	CCCUCUUUAU	GCUCCUUGCU	CUUUCUGCAU	GUGUUGCUAA	CGCGACAAUU	180
UUCCCUCAAU	GCUCACAAGC	UCCUAUAGCU	UCCCUUCUUC	CCCCAUACCU	UCCAUCAAUG	240
AUAGCUUCAG	UAUGUGAAAA	CCCAGCUCUU	CAGCCCUAUA	GGCUCCAACA	AGCAAUCGCA	300
GCAAGCAACA	UACCUUUAUC	ACCCUUGUUG	UUUCAACAAU	CGCCAGCCCU	AUCUUUGGUG	360
CAGUCAUUGG	UACAAACCAU	CAGGGCACAG	CAGCUGCAGC	AACUCGUGCU	ACCUGUGAUC	420
AACCAAGUAG	CUCUGGCAAA	CCUUUCUCCC	UACUCUCAGC	AACAACAAUU	UCUUCCAUUC	480
AACCAACUGU	CUACACUGAA	CCCUGCUGCU	UAUUUGCAGC	AACAACUAAU	ACCAUUCAGC	540
CAGCUAGCUA	CUGCCUACUC	UCAGCAACAA	CAACUUCUUC	CAUUUAACCA	AUUGGCCGCA	600
CUGAACCCCG	CUGCUUAUUU	GCAGCAGCAA	AUACUACUAC	CAUUUAGCCA	GCUAGCUGCA	660
GCAAACCGUG	CUUCCUUCUU	GACACAGCAA	CAGUUGCUGC	CUUUCUACCA	GCAGUUUGCG	720
GCUAACCCCG	CAACCCUCUU	ACAACUACAA	CAAUUGUUGC	CCUUUGUCCA	ACUUGC UUUG	780
ACAGACCCAG	CGGCCUCCUA	CCAACAACAC	AUCAUUGGUG	GUGCCCUCUU	UUAGAUUGCU	840
UAUUAGUUGU	AAJUCAAUAA	UAAAGUUUUU	UGGAUGAUGU	AUGUGGCCAA	CCAGAAAUAA	900
GAAGUUACAU	UUCAGAUUUU	U				921

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGAGUGAUUC	UUUAAACCGA	UUUUAACACA	AGUUAACCAC	ACUAAAAUUA	ACAUUGGUGA	60
AUCGUGCCAU	GAUUUUUUUC	UAGUGCAAAA	UAGCCAAACC	AAGCAAAACA	UAUGUGGCUA	120
UCGUUACACA	UGUGUAAAGG	UAUUGCAUCA	CACCAUUGUC	ACCCAUGUAU	UUGGACAAUA	180
CCGAGAGGAA	AAACCACUUA	UUUAUUGUAU	UUUAUCAAGU	UUUUCUUGCU	UACGUUAAAA	240
UUUAUACCCA	ACAAAGUAAU	CACUAAAUGU	CAAAACCAAC	UAGAUACCAU	GUCAUCUCUA	300

CCUUAUCUUA	CUAAUAUUCU	UUUGGCAAAA	UCGAAAAUUA	AUCUUGCACA	AGCACAAGGA	360
CUGAGAUGUG	UAUAAAUAUC	UCUUAGAUUA	GUAGAUAAUA	UAUCGCACAU	AUUAUUGAGA	420
CCAACUAGCA	ACAUAGAAAG	CACAAUAUUG	UACCAAUAAU	GGCAGCCAAA	AUAUUUUGCC	480
UCAUUAUGCU	CCUUGGUCUU	UCUGCAAGUG	CUGCUACGGC	GAGCAUUUUC	CCGCAAUGCU	540
CACAAGCUCC	UAUAGCUUCC	CUUCUUCCCC	CAUACCUCUC	ACCAGCGAUG	UCUUCAGUAU	600
GUGAAAAUCC	AAUUCUUCUA	CCCUCACAGGA	UCCAACAGGC	AAUCGCAGCA	GGCAUCUUAC	660
CUUUUAUACC	CUUGUUCUC	CAACAAUCAU	CAGCCCUAUU	ACAGCAGUUA	CCUUUGGUGC	720
AUUUAUUGGC	ACAAAACAUC	AGGGCACAAC	AACUACAACA	ACUCGUGCUA	GCAAACCUUG	780
CUGCCUACUC	UCAGCAACAG	CAGUUACCUU	UGGUGCAUUU	GUUGGCACAA	AACAUCAGGG	840
CACAACAACU	ACAACAACUC	GUGCUAGCAA	ACCUUGCUGC	CUACUCUCAG	CAACAACAGU	900
UUCUGCCAUA	CAACCAACUA	GCUGCAUUGA	ACUCUGCUGC	UUUUUUGCAG	CAACAACAAC	960
UACUACCAUU	CAGCCAGCUA	GCUGCUGCCU	ACCCCGGCA	AUUUCUCCA	UUCAACCAAC	1020
UGGCAGCAUU	GAACUCUCAU	GCUUAUGUAC	AACAACAACA	ACUACUACCA	UUCAGCCAGC	1080
UAGCUGCUGU	GAGCCUGCU	GCCUUCUUGA	CACAGCAACA	UUUGUUGCCG	UUCUACCUGC	1140
ACACUGCGCC	UAACGUUGGC	ACCCUCUUAC	AACUGCAACA	AUUGCUGCCA	UUCGACCAAC	1200
UUGCUUUGAC	AAACCCAGCA	GUGUUCUACC	AACAACCCAU	CAUUGGUGGU	GCCCUCUUUU	1260
AGAUUGCUIA	UGAGUUUAUAG	UUCAAUAUA	AAGUUUUUUU	UGCUGAUUUU	UGUGGCUUCC	1320
CAGAAUAAG	AAAGUACAUU	UCUAGAUUCU	UAUGUGCUUC	UAGU		1364

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACCAACAAG CAACATAGA

19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGCAGGG TTCAGTGTAG ACA

23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

22

TCTAGGAAGC AAGGACACCA CC

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

22

GCAAGACCGG CAACAGGATT CA

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

21

GCACTTCTCC ATCACCACCA C

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TATCCCCTTT CCAACTTTCA G